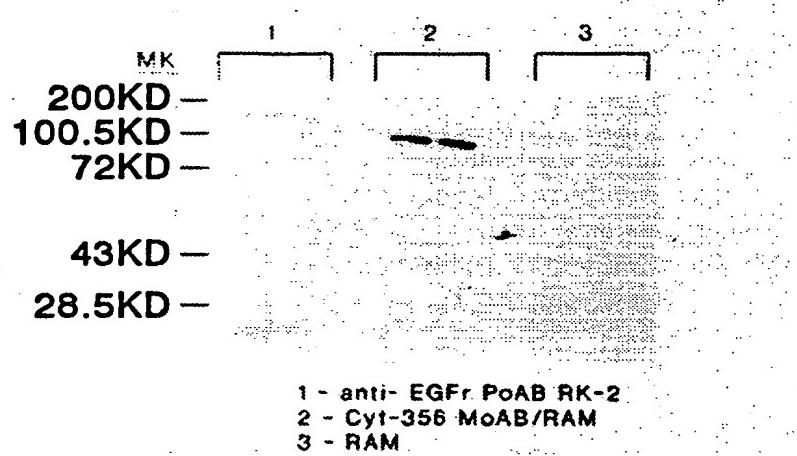


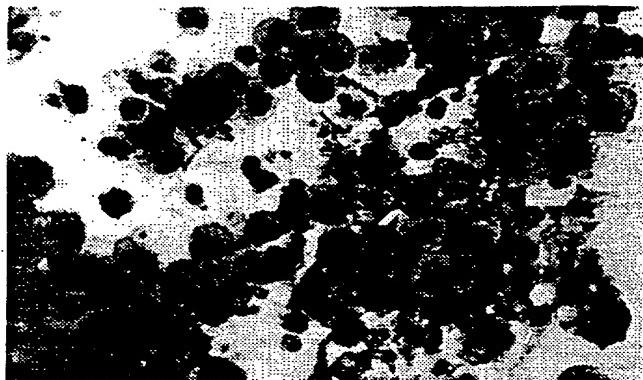
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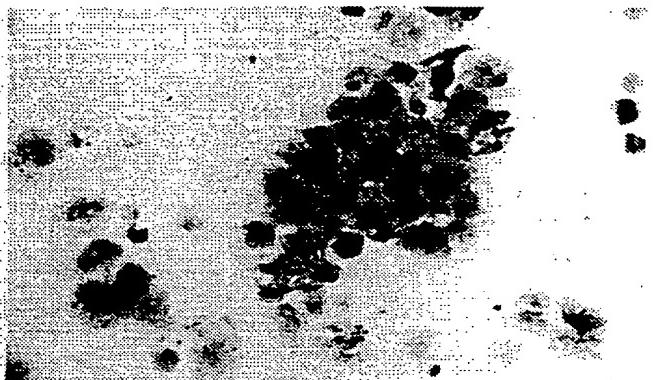
**FIGURE 1**

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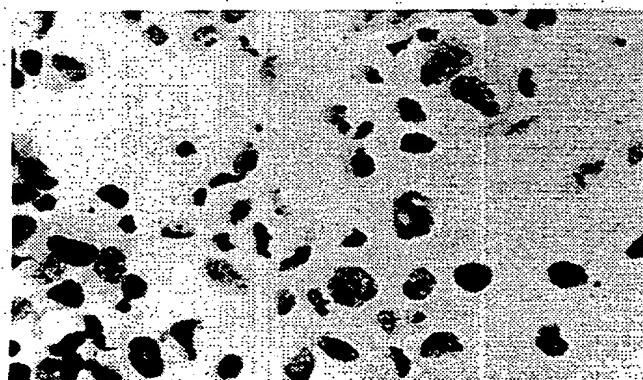
**FIGURE 2A**



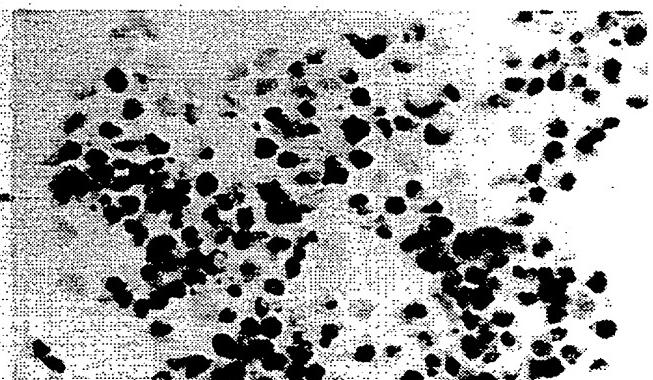
**FIGURE 2B**

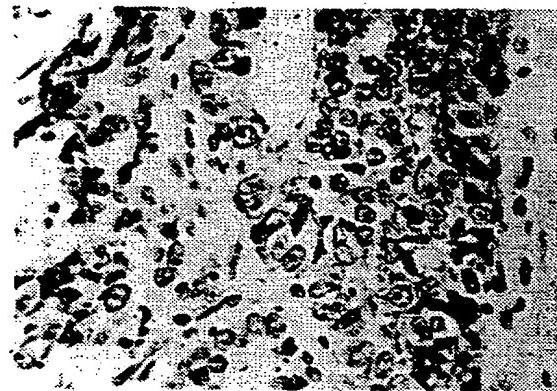
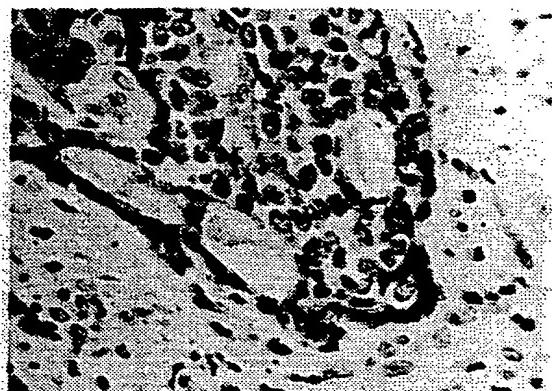
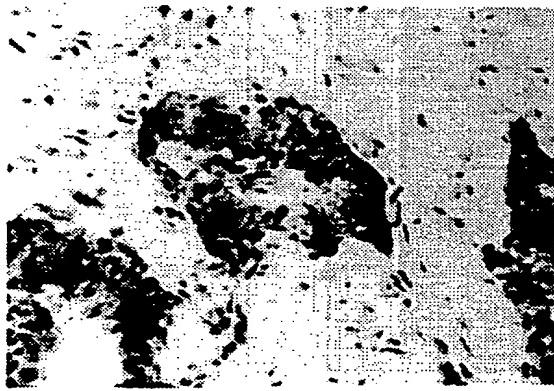
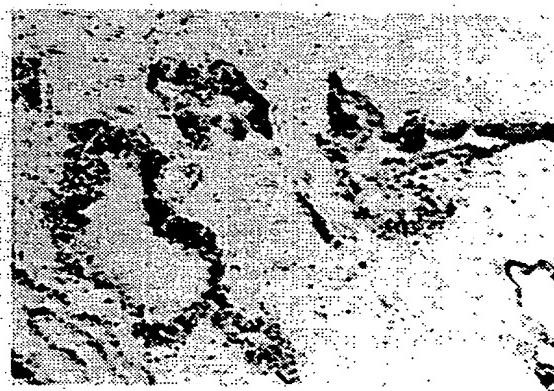


**FIGURE 2C**



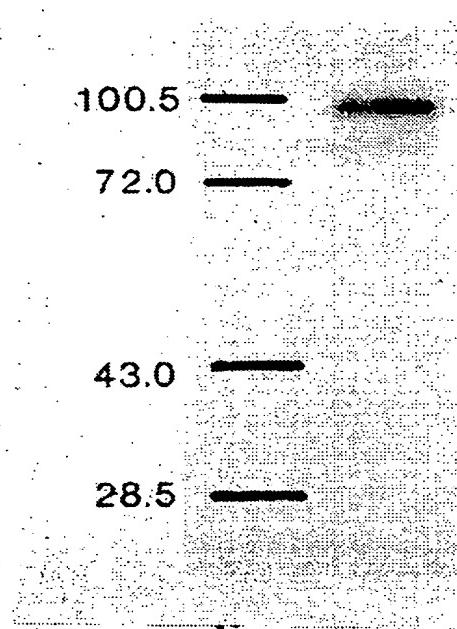
**FIGURE 2D**



**08/466381****3/48****FIGURE 3A****FIGURE 3B****FIGURE 3C****FIGURE 3D**

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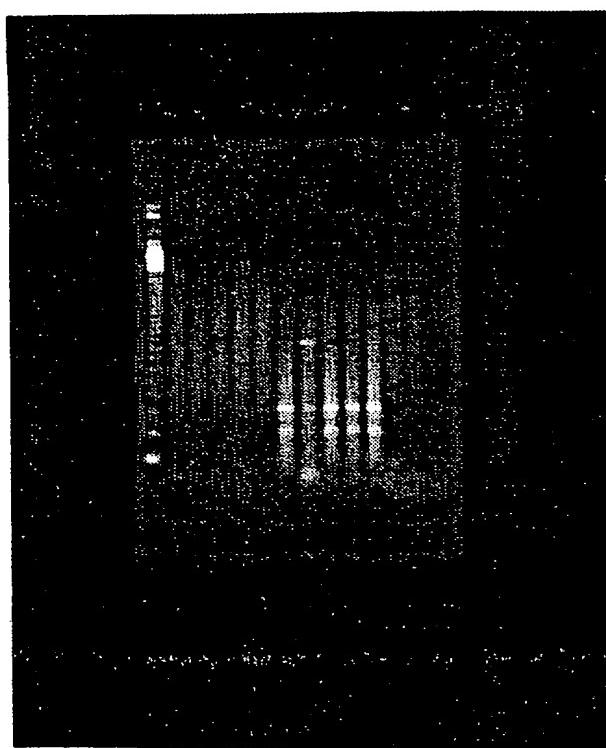
**FIGURE 4**



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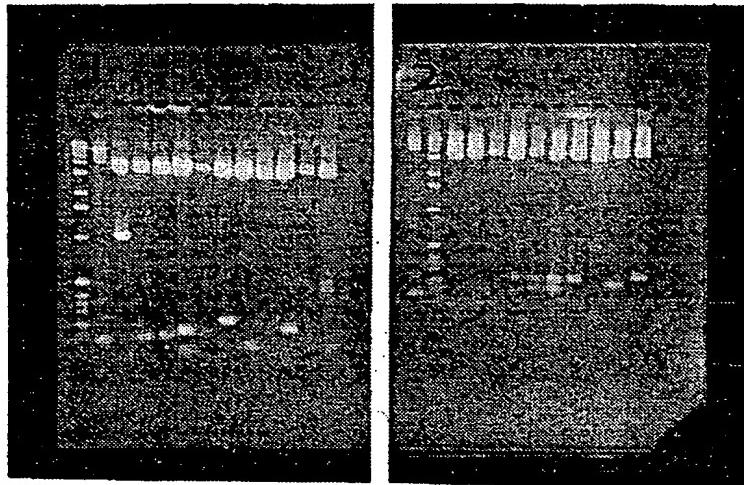
**FIGURE 5**



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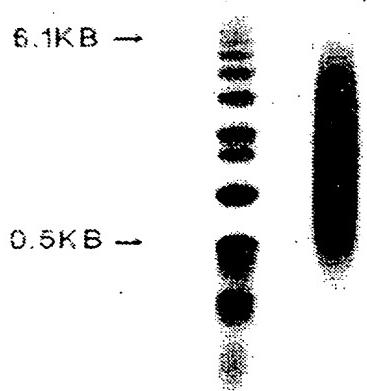
**FIGURE 6A    FIGURE 6B**



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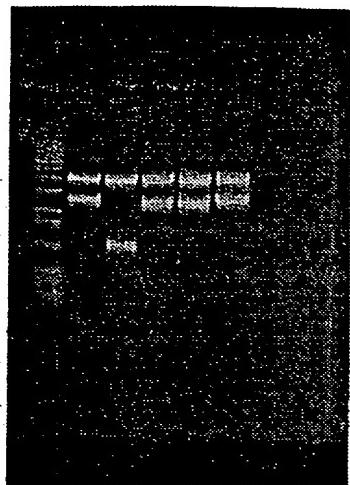
**FIGURE 7**



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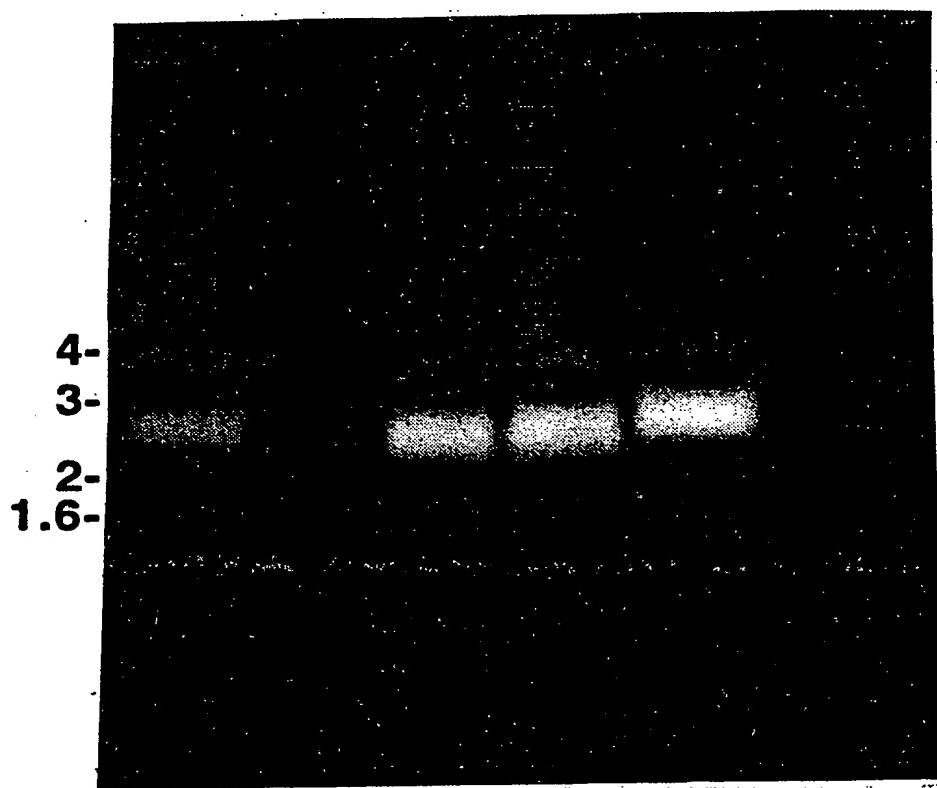
**FIGURE 8**



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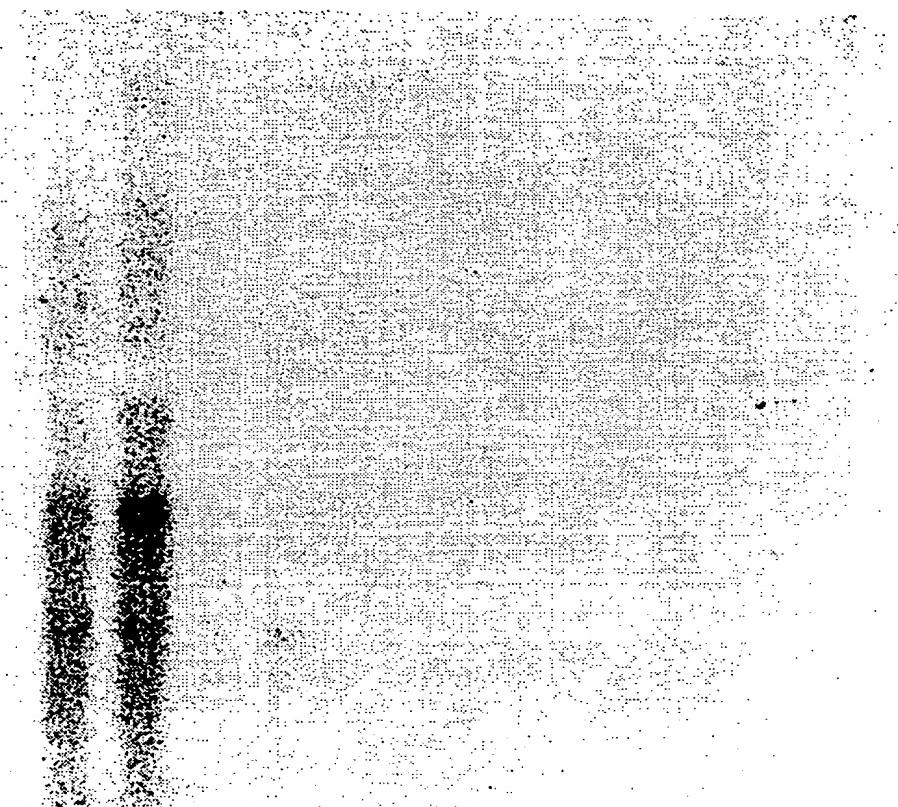
**FIGURE 9**

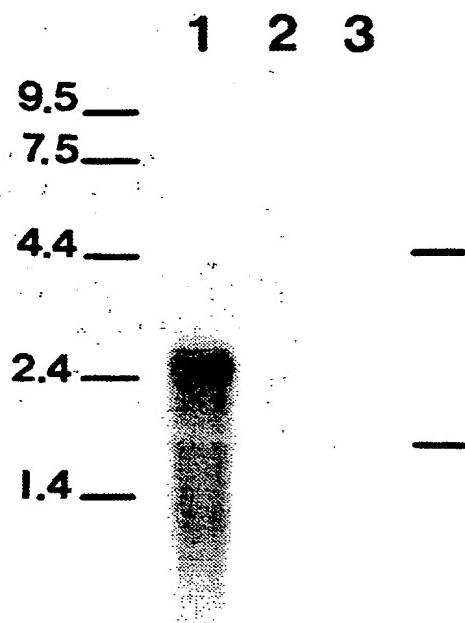


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**FIGURE 10**

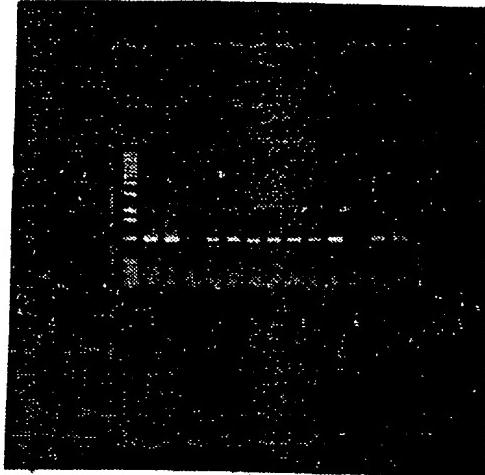


**13/466381****11/48****FIGURE 11**

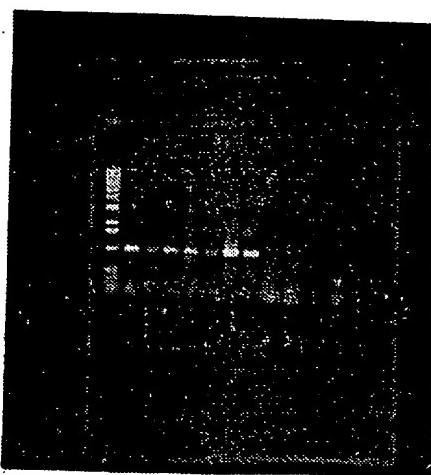
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**FIGURE 12A**



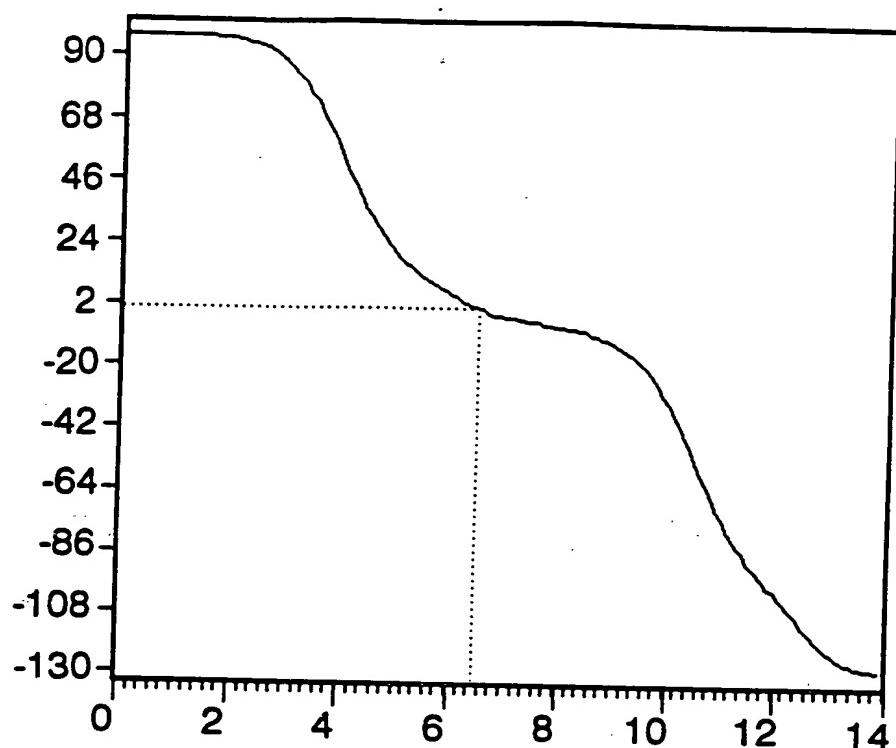
**FIGURE 12B**



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## FIGURE 13



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## FIGURE 14-1

Done on sequence PMSANTIGEN.  
 Total number of residues is: 750.  
 Analysis done on the complete sequence.

In Helical	(H) conformation [DC = -75 CNAT ] :	264 AA => 35.2%
In Extended	(E) conformation [DC = -88 CNAT ] :	309 AA => 41.2%
In Turn	(T) conformation [DC = 0 CNAT ] :	76 AA => 10.1%
In Coil	(C) conformation [DC = 0 CNAT ] :	101 AA => 13.4%

Sequence shown with conformation codes.

---

Consecutive stretch of 5 or more residues in a given conformation are overlined.

1    H H H H H H H H H H E E E T T E E E E E E E E E E E  
 31    E E E E E H H H H H C C C C T H H H H H H H H H H H  
 61    H H H H H H H H H H E E E T T E E E C C C C C C C C

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**FIGURE 14-2**

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FIGURE 14-3

451 E E C C E T E E E E E E E H H H H H H H H  
481 H C C H  
511 E E E C C C C C C E E E H H H H H H H H H H H H H H  
541 T E T T T T C E  
571 H H H E H E  
601 H  
631 H  
661 E E H  
691 E E E T C C C C T E E E E E E E E E E E E E E E E E  
721 C H

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FIGURE 14-4

Semi-graphical output.  
=====

Symbols used in the semi-graphical representation:

Helical conformation: X  
 Turn conformation: >  
 Coil conformation: \*

The diagram shows a semi-graphical representation of a protein sequence. The sequence is aligned with vertical tick marks at positions 10, 20, 30, 40, and 50 on the left, and 60, 70, 80, 90, and 100 on the right. The sequence itself is: MNLLIHETD~~S~~AVATARRPRWLCAGALVLAGGFFFLIGFWFIKSSNEAT. The symbols used are: X for helix (e.g., at positions 10-20), > for turn (e.g., at positions 20-30), \* for coil (e.g., at positions 30-40), and - for extended conformation (e.g., at positions 40-50). Below the sequence, two dashed lines indicate regions of homology or comparison: one from position 50 to the end of the sequence, and another from position 60 to the end.

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FIGURE 14-5

XXXXXXXXXX-->----\*-\*-\*-\*XXXXXXX-X\*---  
XXXXXXXXXX-->----\*-\*-\*-\*XXXXXXX-X\*---

110        120        130        140        150  
|            |            |            |            |  
KEFGLDSVELAHYDVLLSYPNKTHPNYISIINEDGNEIFNTSLFEP PPPG

->>\*-\*XXXXXXX----->>\*-\*----->>\*-\*-\*->>  
->>\*-\*XXXXXXX----->>\*-\*----->>\*-\*X----->>\*-\*-\*->>

160        170        180        190        200  
|            |            |            |            |  
YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKI

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**FIGURE 14-6**

>----->-\* \*->\* \*-\*-----  
 >----->-\* \*->\* \*-\*-----  
 >----->-\* \*->\* \*-\*-----  
 >----->-\* \*->\* \*-\*-----  
  
 210      220      230      240      250  
 |           |           |           |  
 VIARYGKVFRGNKVKNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNLPG  
  
 >----->-\* \*XXXXXX----->----->----->-\* \*->  
 >----->-\* \*XXXXXX----->----->----->-\* \*->  
  
 260      270      280      290      300  
 |           |           |           |  
 GGVQRGNILNLNGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIGYY  
  
 >\*----->>>\*-\*\*-----XX-----\*-----  
 >\*----->>>\*-\*\*-----XX-----\*-----  
  
 310      320      330      340      350  
 |           |           |           |  
 DAQKLLEKMGGSAPPDSSWRGSLKVPYNVGPGFTGNFSQTQKVKMHHISTN  
  
 XXXXXX->>>\* \*-\*>->>->-----\*-----\*-----\*-----  
 XXXXXX->>>\* \*-\*>->>->-----\*-----\*-----\*-----  
  
 360      370      380      390      400  
 |           |           |           |  
 EVTRIYNVIGTLRGAVEPDRYVILLGGHRDSWVFGGIDPQSGAAVVHEIVR

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FIGURE 14-7

----- \* \* \* >-----> \* \* \* > \* \* XXX-----XX  
 ----- \* \* \* >-----> \* \* \* > \* \* \* > \* \* XXX-----XX  
 ----- \* \* \* >-----> \* \* \* > \* \* \* > \* \* XXX-----XX

410            420            430            440            450  
 |                |                |                |  
 SFGTILKKEGWRPRRTILFASWDAEEFGLLGSTEWAEENSRLLQERGVAYI

XXX\* \* \* >>> \* \* \* >-----> \* XXXXXXXX\* \* \* \* XXXXXXXX-----  
 XXX\* \* \* >>> \* \* \* >-----> \* XXXXXXXX\* \* \* \* XXXXXXXX-----  
 XXX\* \* \* >>> \* \* \* >-----> \* XXXXXXXX\* \* \* \* XXXXXXXX-----

460            470            480            490            500  
 |                |                |                |  
 NADSSIEGNYTLRVVDCTPLMYSLVHNLTKEKSPDEGFEGKSLYESWTK

----- \* \* ----->>-----> \* XXXXXXXX\* \* XXXXXXXX>>>  
 ----- \* \* ----->>-----> \* XXXXXXXX\* \* XXXXXXXX>>>

510            520            530            540            550  
 |                |                |                |  
 SPSPEFSGMPRISKLGSGNDFFEVFFQRLGIASGRARYTKNWETNKFSGYP

\* \* \* >-----> \* \* \* \* -----> \* \* \* >-----> \* >----->  
 \* \* \* >-----> \* \* \* \* -----> \* \* \* >-----> \* >----->

560            570            580            590            600  
 |                |                |                |  
 -----

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FIGURE 14-8

LYHSVYETYELVEKFYDPMFKYHILTVAQVRGGMVFELANSIVILPPFDCCRDY  
 -----X\*\*\*\*\*-----X----->XXX  
 -----X\*\*\*\*\*-----X----->XXX  
 -----X\*\*\*\*\*-----X----->XXX

610            620            630            640            650  
       |            |            |            |  
 AVVLRKYADKIVSISMKHPQEMKTYSVSFDLSLFSAVKNFTEIASKFSERL

XXXXXX-----X\*\*-----X----->XXXXXX  
 XXXXXX-----X\*\*-----X----->XXXXXX  
 XXXXXX-----X\*\*-----X----->XXXXXX

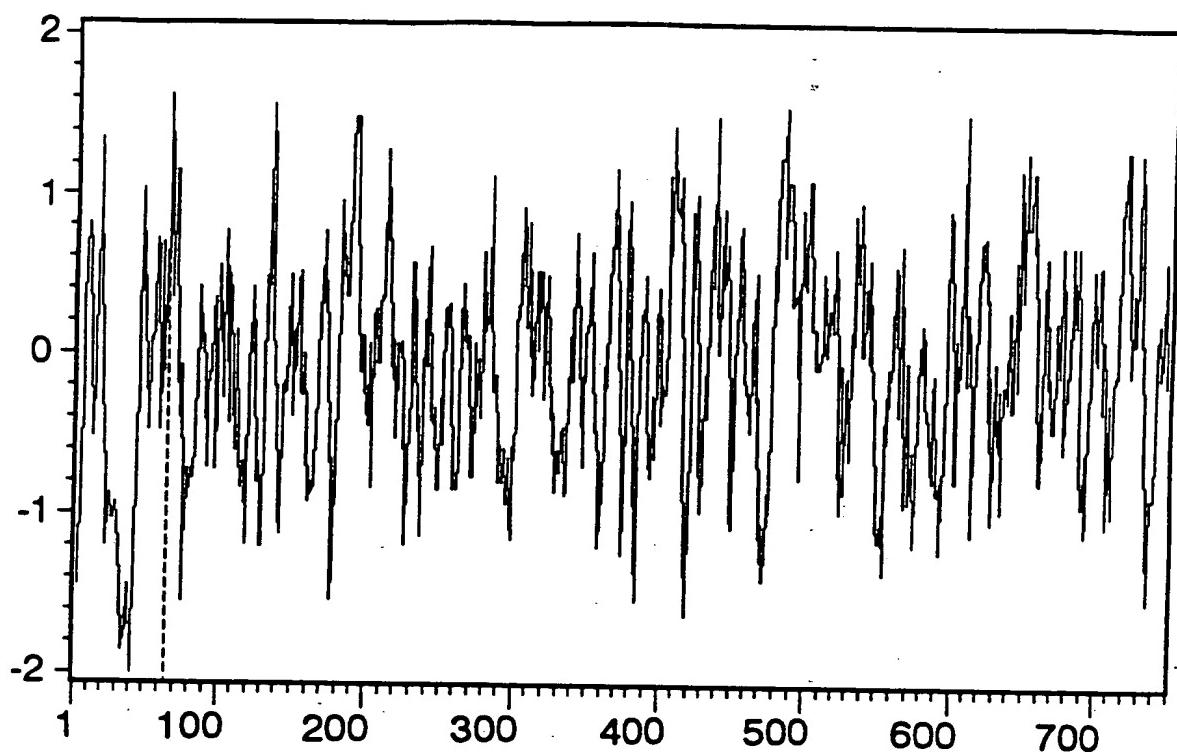
660            670            680            690            700  
       |            |            |            |  
 QDFDKSMPIVLRRMNDQLMCLERAFIDPLGLPDRPFYRHVIYAPSSHINKY

XX>>\*-----XXXXXX----->\* \* \* >----->\* \* \* >  
 XX>>\*-----XXXXXX----->\* \* \* >----->\* \* \* >

710            720            730            740            750  
       |            |            |            |  
 AGESFPGIYDALFDIESKVDPSSKAWGEVKRQIYVAAFTVQAAAETLSEVA  
 ----->--XXXXXX\* \* \* \* XXXXXXXX----->XXXXXX  
 ----->--XXXXXX\* \* \* \* XXXXXXXX----->XXXXXX

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**FIGURE 15A**

**FIGURE 15B**

\*\*\*\*\*  
 \* PREDICTION OF ANTIGENIC DETERMINANTS \*  
 \*\*\*\*\*

Done on sequence PMSANTIGEN.  
 Total number of residues is: 750.  
 Analysis done on the complete sequence.

The method used is that of Hopp and Woods.  
 The averaging group length is: 6 amino acids.  
 -> This is the value recommended by the authors <-

The three highest points of hydrophilicity are:

( 1 )	Ah= 1.62 :	From	63 to	68 :	Asp-Glu-Leu-Lys-Ala-Glu
( 2 )	Ah= 1.57 :	From	132 to	137 :	Asn-Glu-Asp-Gly-Asn-Glu
( 3 )	Ah= 1.55 :	From	482 to	487 :	Lys-Ser-Pro-Asp-Glu-Gly

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100% of the cases assigned to a known antigenic group. The second and third point gave a proportion of 33% of incorrect predictions.

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The best scores are:  
**CHKTFER** G. gallus mRNA for transferrin receptor  
**RATTRFR** Rat transferrin receptor mRNA, 3' end.  
**HUMTFR** Human transferrin receptor mRNA, complete cd

**FIGURE 16-1**

initn	initl	opt
203	120	321
164	164	311
145	145	266

**CHKTFER** G.gallus mRNA for transferrin receptor  
51.9% identity in 717 nt overlap

	203	120	321
CHKTFER	1020	1030	1040
pmssgen	TGTCCAGCGTGGAAATATCCTAAATCTGAATG	GCGACATGCCAACCATTCGG	CAGGAGACCCCTTGAAACTTG
	990	1000	1010
CHKTFE	1080	1090	1100
pmssgen	CCCAGGAAATGAATATGCTTATAGGGCTTATTG	CAAGGCTGAATTGCAGAGG	GCTCTGGTCTGGCTTCCAA
	1050	1060	1070
CHKTFE	1140	1150	1160
pmssgen	TCCTGTTCAATTGGATACTATGATGCACAGA	AGGCTCCTAGAAAAATGGGT	GGCTC
	1110	1120	1130
CHKTFE	1120	1130	1140
	1150	1160	1170
	1160	1170	1180
	1170	1180	1190

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FIGURE 16-2

1200	1210	1220	1230	1240	1250
pmsgen	AGCACCAACGATAGCGAGGGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG				
:	: : : : :	: : : :	: : :	: : :	: : :
CHKTFE	CACATGCTCTGA-AG--GTTGGAAAGGTGGCATCCA---TTCCCTGTAAGGT--GAC--AA				
1170	1180	1190	1200	1210	

1260	1270	1280	1290	1300	1310
pmsgen	CTTTACTGGAAACTTTCTACACAAAAAAGTCAGAGATGGCACATCCACTCTACCAATGAACT				
:	: : : : :	: : :	: : :	: : :	: : :
CHKTFE	CAAAGCAGGAGA---GCCAGA-TAATGGTGAAGAACTAGATGTGAACAATTCCATGAAAGA				
1220	1230	1240	1250	1260	

1320	1330	1340	1350	1360	1370
pmsgen	GACAAGAATTACAAATGTTGATAGGTACTCTCAGAGGAGGACTGGAACCAGACAGATATGT				
:	: : : : :	: : :	: : :	: : :	: : :
CHKTFE	CAGGAAGAATTCTGAACATCTTCGGTGCTATCCAGGGATTTGAAGAACCTGATCCGGTATGT				
1270	1280	1290	1300	1310	1320

1380	1390	1400	1410	1420	1430
pmsgen	CATTCTGGGAGGTCAACCGGGACTCATGGGTATTGACCC'TCAGAGTGGAGC				
:	: : : : :	: : :	: : :	: : :	: : :
CHKTFE	TGTGATTGGAGCCCCAGAGAGACTCCCTGGGGGGCTAAAGCTGGCAGTGGAAC				
1330	1340	1350	1360	1370	1380

FIGURE 16-3

<b>pmsgen</b> ::::: ::::: ::::: ::::: <b>CHKTFE</b> 1390	1440      1450      1460      1470      1480      1490 AGCTGTTGTCATGAAATTGTGAG---GAGCTTGGAAACACTGAAAAAGGAAGGGTCCAG ::::: ::::: ::::: ::::: TGCTATATTGTTGGAACCTGCCGTGTGATCTCAGACATAGTGAACAAACGAGGGCTACAA 1400      1410      1420      1430      1440	1500      1510      1520      1530      1540      1550 ACCTAGAAGAACAAATTGTTGCAAGCTGGATGCAGAAGAAATTGGTCTTCTGGTTC ::::: ::::: ::::: ::::: <b>CHKTFE</b> 1450	1460 ACCGAGCGAAGGCATCATCTTGCTGGAGTAGCTGCAGGAGACTACGGAGCTGTGGGTGC 1470      1480      1490      1500	1560      1570      1580      1590      1600      1610 TACTGACTGGCAGGGAGAATTCAAGAACCTCCTTAAGAGCGCTGGCTTATATTAA ::::: ::::: ::::: ::::: <b>CHKTFE</b> 1510	1520 1530 1540 1550 1560 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670	26/48 466381
--	---	---	---	--	--	-----------------

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FIGURE 16-4

1680      1690      1700      1710      1720      1730  
pmsgen TACAGCTTGGTACACAACTAACAAAAGAGCTGAAAGCCCTGATGAAGGCTTGTGAAGGC  
::: ::    :: :    :: :    :: :    :: :    :: :  
CHKTFE TATATGCTGGGGACTATTATGAAGGGGGTGAAGAATCCAGCAGCAGTCTCAGAGGC  
1630      1640      1650      1660      1670      1680

1740      1750      1760      1770      1780      1790  
pmsgen AAATCTTTATGAAAGTTGGACTAAAAAAGTCCTTCCCCAGACTTCAGTGGCATGCC  
::: ::    :: :    :: :    :: :    :: :  
CHKTFE ----CTCTATAACAGACTTGGCCCAGACTGGGTAAAAGCAGTTGTTCCCTGGCCTGGGA  
1690      1700      1710      1720      1730

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## FIGURE 16-5

RATTRFR Rat transferrin receptor mRNA, 3' end.  
55.5% identity in 560 nt overlap

1210	1220	1230	1240	1250	
mssgen CCACAGATGCCGAGGAAGTCTCAAAGTGCCTACAATGTTGGACCTGGCTT-					28/48
::: :::: :::: :::: :::: :::					
RATTRF TGCAGAAAAGCTATTCAAAACATGGAAGGAAACTGTCCCTAGTTGGAATAATAGATTC					
610	620	630	640	650	660
1260	1270	1280	1290	1300	1310
mssgen -TACTGGAAACTTTCTACACAAAAGTCAGATGCCACATC-CACTCT-ACCAATG----					
::: :::: :::: :::: :::					
RATTRF CTCATGTAAGCTGGAACTTCACAGAATCAAATGTGAAGCTCACTGTGAACAAATGTACT					
670	680	690	700	710	720

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FIGURE 16-6

1320	1330	1340	1350	1360	1370
pmsgen	--AAGTGACAAGAATTACAATGTGATAAGGTACTCTCAGGGAGCCAGTGGAAACCAGACAG				
:	::	::	::	:	:
RATTRF	GAAAGAACAAAGAATTACCTAACATCTTGGCGTTATTAAAGCTATGAGGAACCAGACCG				
730	740	750	760	770	780

1380	1390	1400	1410	1420	1430
pmsgen	ATATGTCATTCTGGGAGGTCACCGGGACTCATGGGTGTTGCTGGTATTGACCCCTCAGAG				
:	:	:	:	:	:
RATTRF	CTACATTGTTAGGAGCCCCAGAGAGACGGCTTGGGCCCTGGT-GTTGCGAAGTCCAGTG				
790	800	810	820	830	840

1440	1450	1460	1470	1480	
pmsgen	T-GGAGCAGCTGTTCTCATGAAATTGTTGAGGAGCTTGGAAACA-CTGA---AAAAGGAA				
:	:	:	:	:	:
RATTRF	TGGGAACAGGGTCTT-CTCTGAAACTTGCCCAAGTATTCTCAGATATGATTCAAAGAT				
850	860	870	880	890	900

1490	1500	1510	1520	1530	1540
pmsgen	GGGTGGAGACCTAGAACAAATTCTGCAAGGAAGAATTGGTCTT				
:	X:	:	:	:	:
RATTRF	GGATTAGACCCAGCAGGAGTATTATCTTGCAGCTGGACTGCAGGAGACTATGGAGCT				
910	920	930	940	950	960

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FIGURE 16-7

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1550	1560	1570	1580	1590	1600	
pmsgen	CTTGGCTTCACTGAGTGGCCAGGGAGAA	---	TTC	AAAGACTC	CCTCAAG	GCGTGGCGTG
	:::::	:::::	X	:::::	:::	:::
RATTRF	GTTGGTCCGA	CTGAGTGGCTGGAGGGTAC	CTTCA	TGCATCTAAAG	--GCTTTC	
	980	990	1000	1010	1020	
1610	1620	1630	1640	1650	1660	
pmsgen	GCTTATATTAA	TGACTCATCTATA	GAAGGAA	ACTA	-CACTCTGAGAGTTGATTGTAC	
	:::::	:::::	:::	:::	:::	:::
RATTRF	ACTTACATTAA	AT-CTGGATAAA	AGTCGTCC	CTGGTACTAGCA	AACTTC	CAAGGTTCTGCCAG
	1030	1040	1050	1060	1070	1080
1670	1680	1690	1700	1710	1720	
pmsgen	ACCGCTGATGTA	CAGGCTGGTACACA	ACCTAACAA	AAGAGCTGAAAAGC	-CCTGATGAAAG	
	:::::	:::::	:::	:::	:::::	:::::
RATTRF	CCCCCTATTATAC	ACTTATGGGAAGATA	ATGGCAAGGA	--CGTAAAGCATCCGA	---	
	1090	1100	1110	1120	1130	

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**FIGURE 16-8**

pmssen	GCTTTGAGGCAAATCTCTTAT-GAA-----AGTTGGACTAAAAAGTCCCTCCCCAG	1750	1760	1770
	::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::			
RATTRF	---TTGATGGAAAATATCTATATCGAAACAGTAATTGGATTAGCAAAATTGAGGAACRTT	1140	1160	1170
pmssen	AGTCAGTGGCATGCCAGATAAGCAAAATTGGGATCTGGAAATGATTTGAGGTGTTCT	1780	1790	1800
RATTRF	CCTTGGACAATGCTGCATTCCCTTCTGCATATTAGGAATCCCAGTAGTTCTTTCT	1200	1210	1220

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FIGURE 16-9

HUMTFR Human transferrin receptor mRNA, complete cd 145 145 266  
 54.3% identity in 464 nt overlap

1230	1240	1250	1260	1270	
pmsgen AGGAAGTCTCAAAGTGCCTACAAATGTTGGACCTGGCTTAC-TGGAAACTTTCTACAC					
HUMTFR TATGCAAGGAGACTGTCCCTCTGACTGCCAACAGACTCTACATGTTAGGATGGTAACCTC					
1140	1150	1160	1170	1180	1190
1280	1290	1300	1310	1320	1330
pmsgen AAAAAGTCAGATGCCACATC-CAACTCT-ACCAATG-----AAGTGACAAGAAATTACAA					
HUMTFR AGAAAGCAAGAATGTGAAGGCTCACTGTGAGCAAATGTGCTGAAAGAGATAAAAATTCTAA					
1200	1210	1220	1230	1240	1250
1340	1350	1360	1370	1380	1390
pmsgen TGTGATAGGTACTCTCAGGGAGCCAGTGGAAACCAGATATGTCATTCTGGGAGGGTCA					
HUMTFR CATCTTGGAGTTATTAAAGGCTTTGTAGAACCACTATGTTGACTATGTTGGGGCCA					
1260	1270	1280	1290	1300	1310
1400	1410	1420	1430	1440	1450
pmsgen CCGGGACTCATGGGTGTTGGTATTGACCCCTCAGAGT-GGAGCAGCTGTTCTCATG					
HUMTFR GAGAGATGCCATGGGGCCCTGGAGGCTGCAAATC-CGGTGTAGGCACAGCTCTCCTATTGA					
1320	1330	1340	1350	1360	1370

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FIGURE 16-10

1460      1470      1480      1490      1500  
 pmsgen AAATTG---TGAGGAGCTTGGAACACTGAAAAGGAAGGGCTGGAGACCTAGAAGAACAA  
 ::::: ::::: ::::: ::::: X::: ::::: ::::: :::::  
 HUMTFR AACTTGGCCAGATGGTCTCAGATATGGTCTAAAGATGGGTTTCAGCCCCAGCAGAACCA  
 1380      1390      1400      1410      1420      1430

1510      1520      1530      1540      1550      1560  
 pmsgen TTTTGTGTTGCAAGGCTGGATGCAGAATTTGGTCTTGTCTACTGAGTGGCGAG  
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::  
 HUMTFR TTATCTTGGCAGTTGGAGACTTGGATCGGTTGGTGCCTACTGAATGGCTAG  
 1440      1450      1460      1470      1480      1490

1570      1580      1590      1600      1610      1620  
 pmsgen A-GGAGAAATTCAAGACTCCTCAAGAGCGTGGCGTGGCTTATAATTGCTGACTCATCT  
 ::::: ::::: ::::: ::::: ::::: ::::: X::: :::::  
 HUMTFR AGGGATACTTTCGTC-CCTGCATTAAAGGCTTCACTTATAATTGATAAAAGCG  
 1510      1520      1530      1540      1550

1630      1640      1650      1660      1670      1680  
 pmsgen ATAGAAGGAAACTACACTCTGAGAGTGTGATTGTACACCGCTGATGTACA-GCTTGCT-AC  
 ::::: ::::: ::::: ::::: ::::: ::::: :::::  
 HUMTFR GTTCTTGGTACCAAGCAACTCAAGGTCTGGCCAGCCCCACTGTTGTACGCTTATTGAG  
 1560      1570      1580      1590      1600      1610

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FIGURE 16-11

1690      1700      1710      1720      1730      1740  
pmsgen ACAACCTAACAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAAGCATAATCCTTATG  
: : : : : :  
1620      1630      1640      1650      1660      1670  
HUMTFR AAAACAATGCCAAATGTGAAGCATCCGGTTACTGGCAATTCTATCAGGACAGCAAC

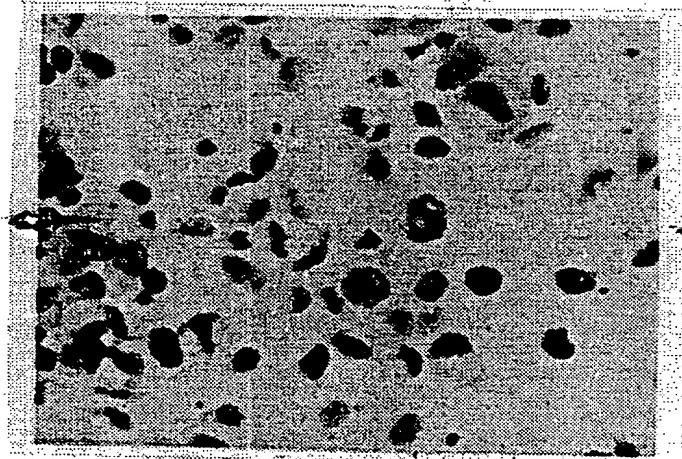
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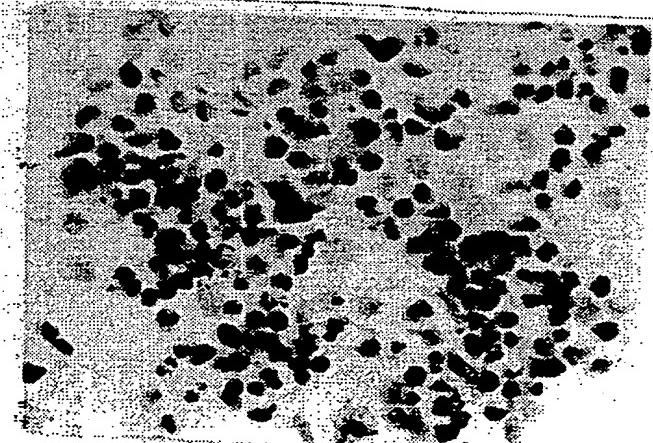
**FIGURE 17A**



**FIGURE 17B**



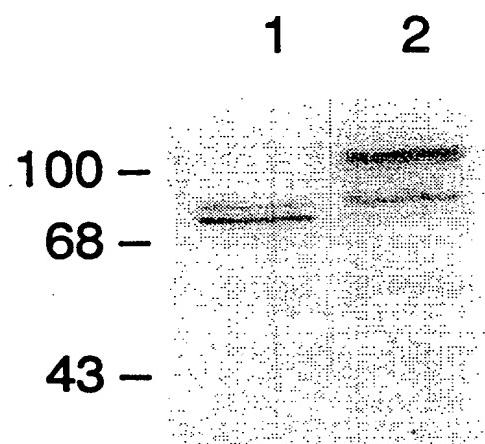
**FIGURE 17C**

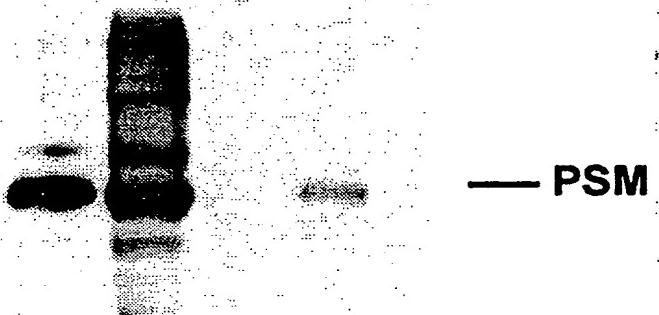


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**FIGURE 18**

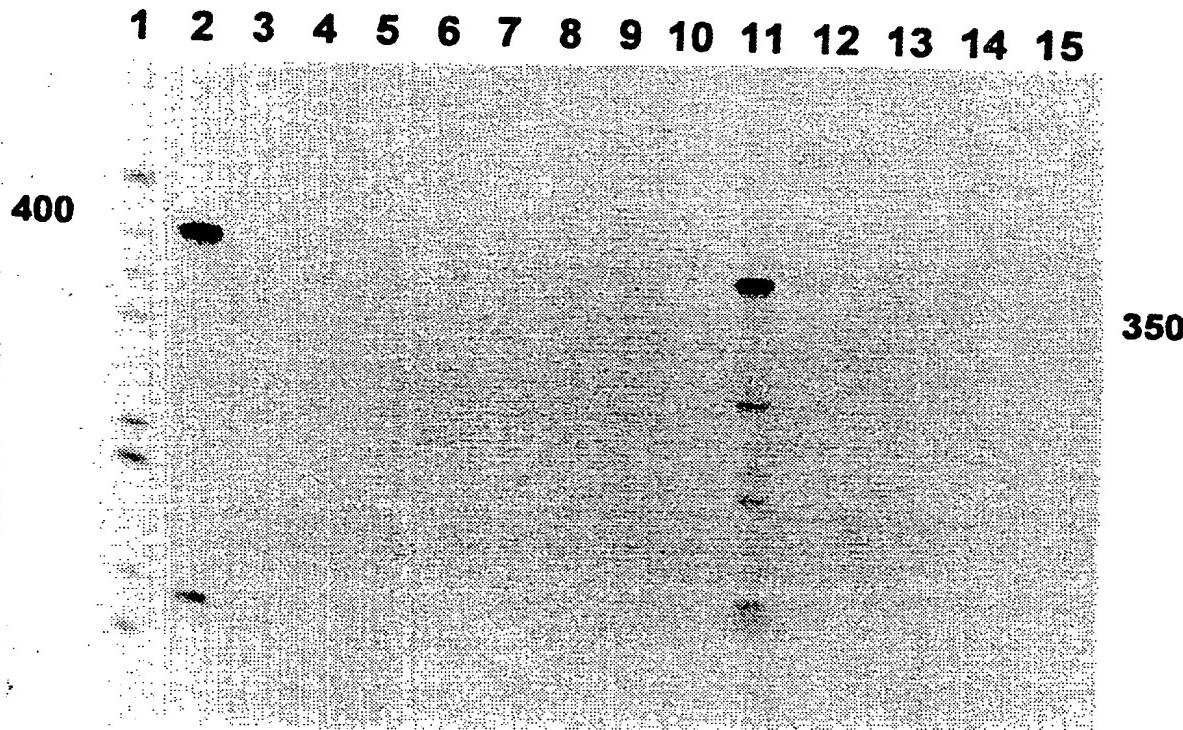


**18/466381****37/48****FIGURE 19****1 2 3 4****200 kDa —****100 kDa —****69 kDa —**

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**FIGURE 20**

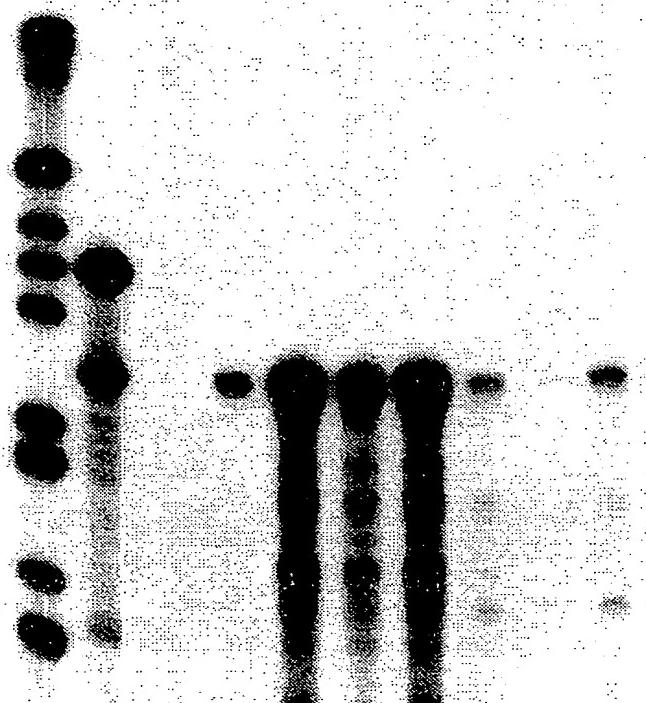


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**FIGURE 21**

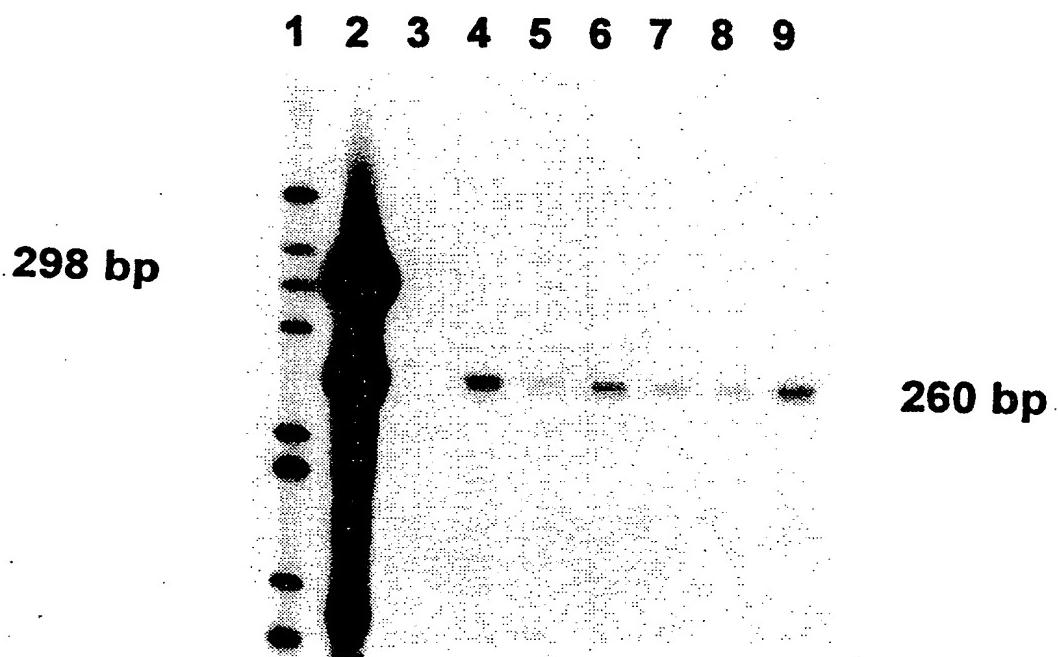
1 2 3 4 5 6 7 8 9 10

**298 bp****260 bp**

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**FIGURE 22**



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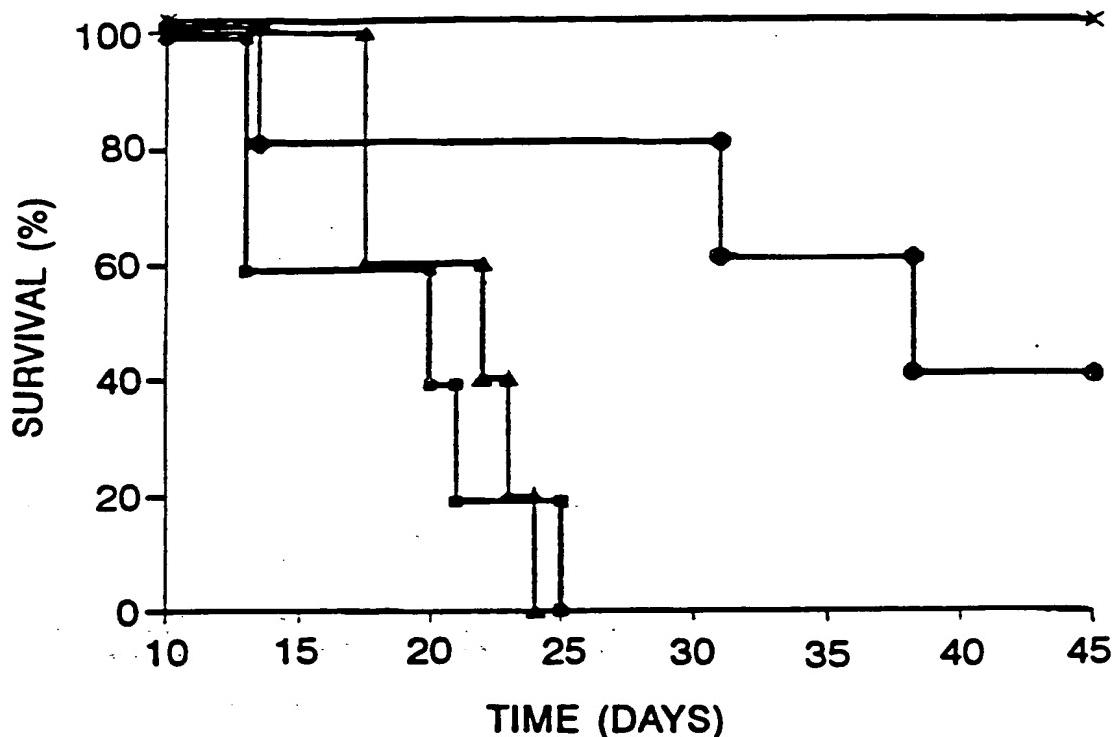
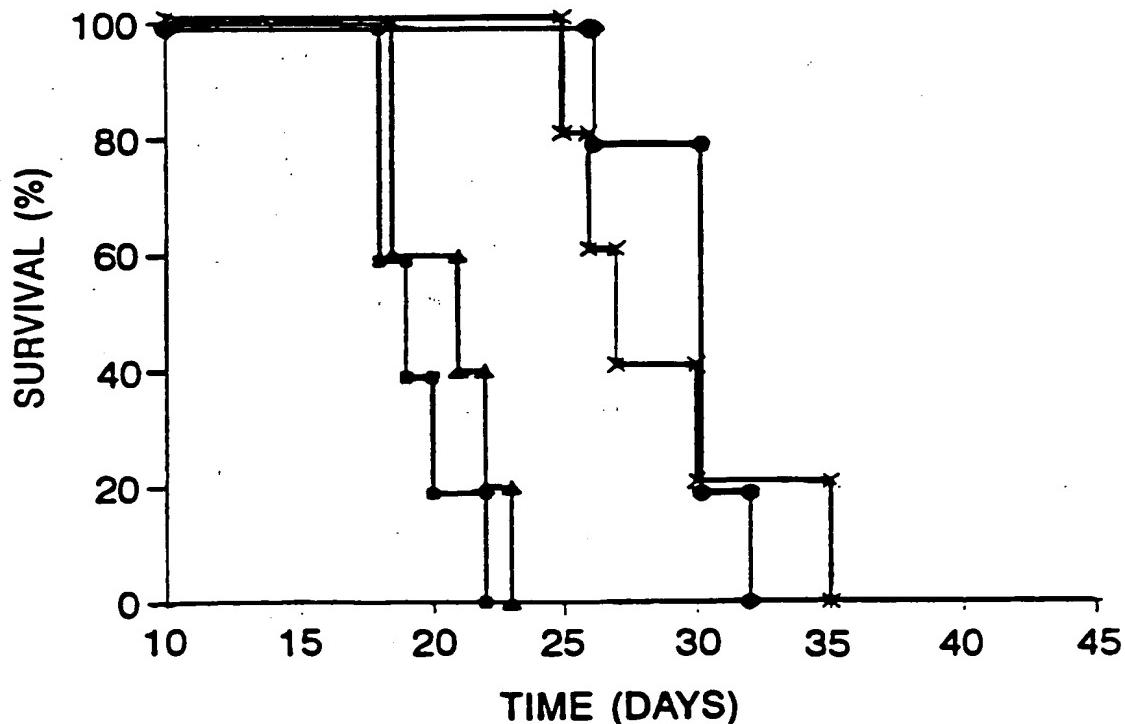
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## FIGURE 23

CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	-	-
R1564 (RAT MAMMARY)	NO	YES	-	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	-	ND
R1564-11-c12	YES	YES	ND	+

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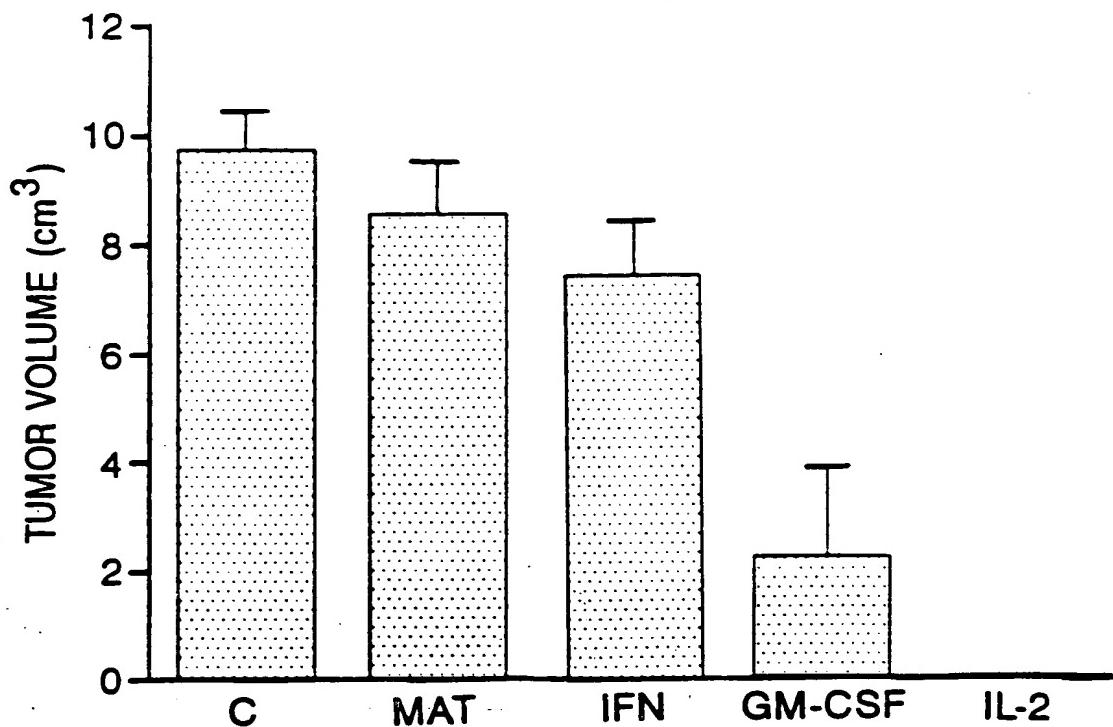
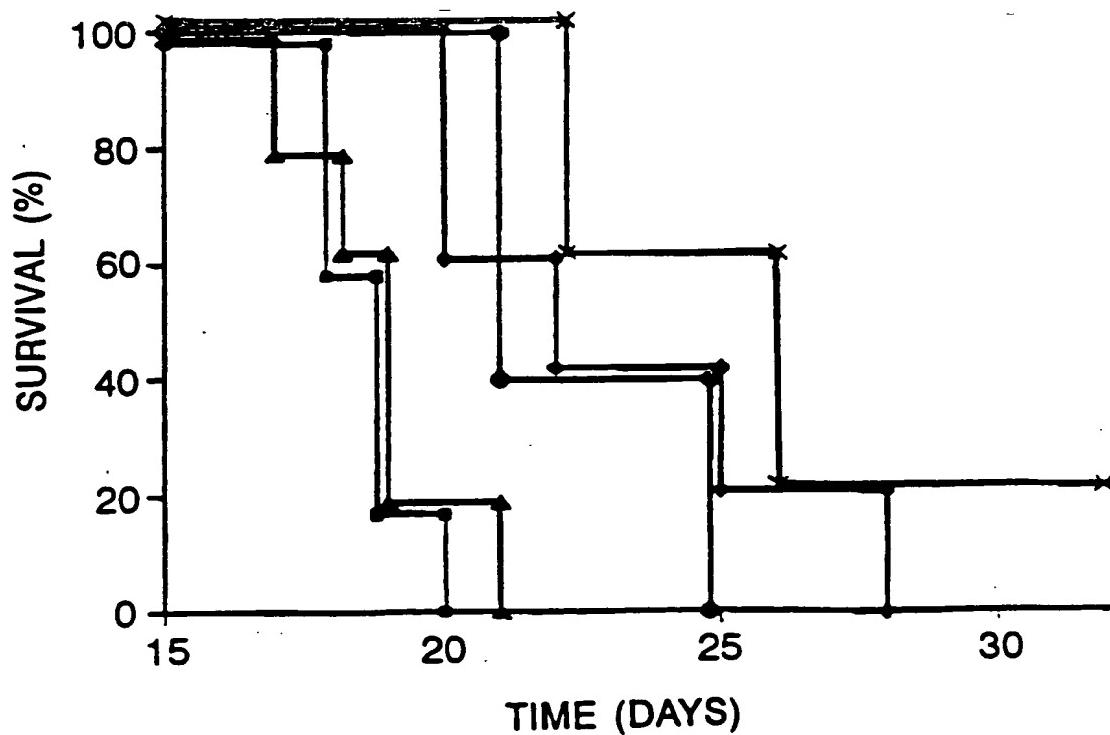
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**FIGURE 24A****FIGURE 24B**

SUBSTITUTE SHEET (RULE 26)

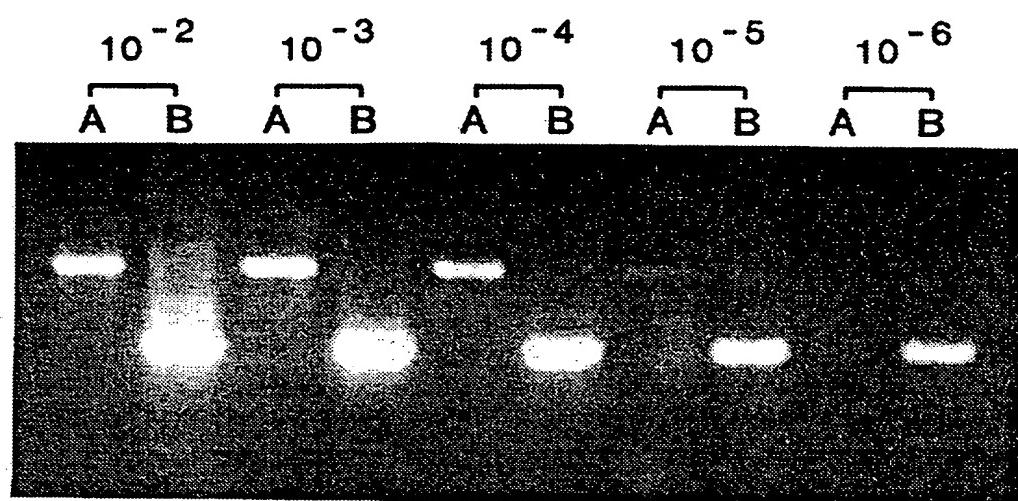
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**FIGURE 25A****FIGURE 25B**

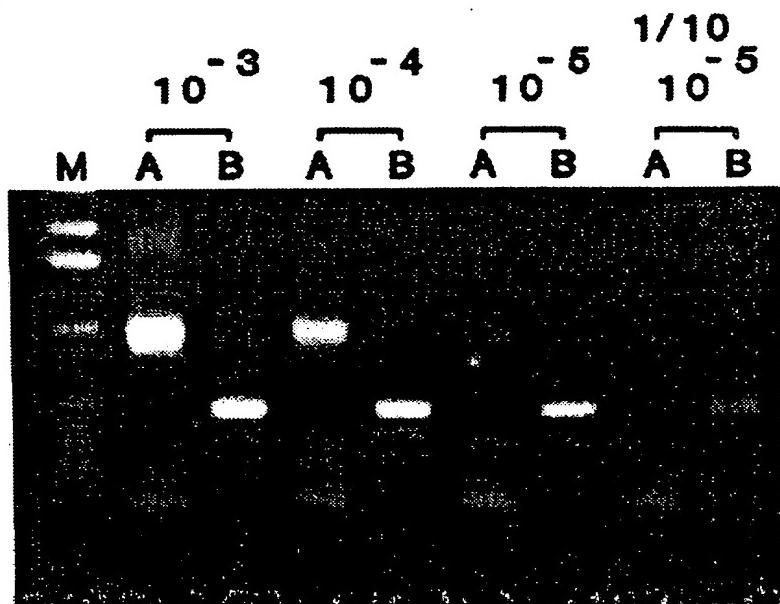
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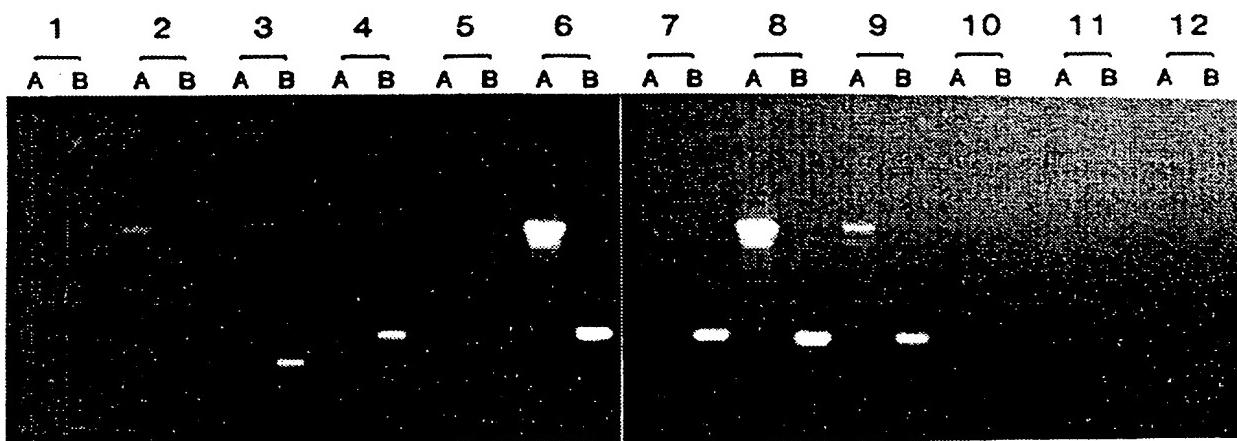
**FIGURE 26**

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FIGURE 27



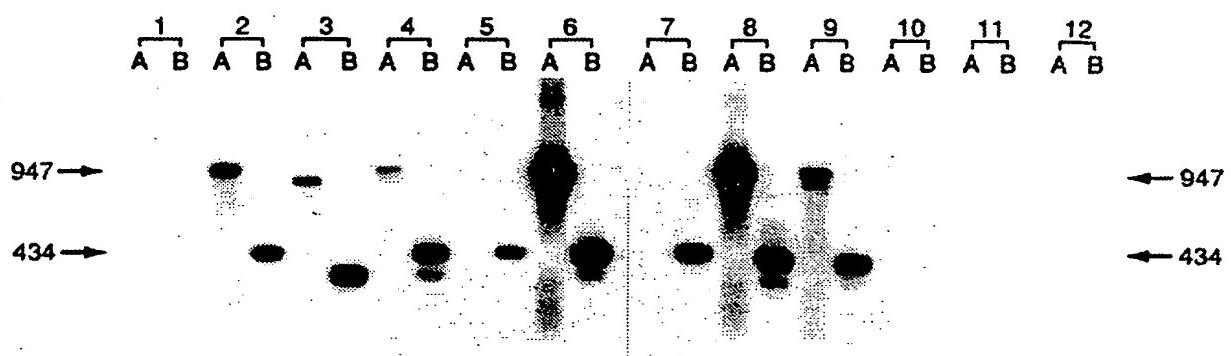
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**46/48****FIGURE 28**

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## FIGURE 29



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## FIGURE 30

Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	-	+
2	T2NoMo	RRP 7/93	6.1	-	-	+
3	T2CNoMo	PLND 5/93	4.5	0.1	-	+
4	T2BNoMo	RRP 3/92	NMA	0.4	-	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	-	+
6	Recur T3	I-125 1986	54.7	1.4	-	+
7	T3ANoMo	RRP 10/92	NMA	0.3	-	+
8	T3NxMo	XRT 1987	7.5	0.1	-	-
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	-
10	D2	S/P XRT Flutamide +Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	-	+
13	T3NoMo	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	-
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	-
15	D1	Proscar + Flutamide	20.8	0.5	-	-
16	T2CNoMo	RRP 4/92	0.1	0.3	-	-